WHAT IS CLAIMED IS:

1. An isolated nucleic acid comprising a genomic, complementary or composite polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

2. The isolated nucleic acid of claim 1, wherein said polynucleotide or a portion thereof is hybridizable with SEQ ID NOs: 9, 13, 42, 43 or a portion thereof at 68 °C in 6 x SSC, 1 % SDS, 5 x Denharts, 10 % dextran sulfate, 100 μg/ml salmon sperm DNA, and ^{32}p labeled probe and wash at 68 °C with 3 x SSC and 0.1 % SDS.

3. The isolated nucleic acid of claim 1, wherein said polynucleotide or a portion thereof is at least 60 % identical with SEQ ID NOs: 9, 13, 42, 43 or portions thereof as determined using the Bestfit procedure of the DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the university of Wisconsin (gap creation penalty - 12, gap extension penalty - 4).

4. The isolated nucleic acid of claim 1, wherein said polypeptide is as set forth in SEQ ID NOs:10, 14, 44 or portions thereof.

5. The isolated nucleic acid of claim 1, wherein said polypeptide is at least 60 % homologous to SEQ ID NOs:10, 14, 44 or portions thereof as determined with the Smith-Waterman algorithm, using the Bioaccelerator platform developed by Compugene (gapop: 10.0, gapext: 0.5, matrix: blosum62).

6. A nucleic acid construct comprising the isolated nucleic acid of claim 1.

7. A host cell comprising the nucleic acid construct of claim 6.

8. A recombinant protein comprising a polypeptide having heparanase catalytic activity.

9. The recombinant protein of claim 8, wherein said polypeptide includes at least a portion of SEQ ID NOs:10, 14 or 44.

10. The recombinant protein of claim 8, wherein the protein is encoded by a polynucleotide hybridizable with SEQ ID NOs: 9, 13, 42, 43 or a portion thereof at 68 °C in 6 x SSC, 1 % SDS, 5 x Denharts, 10 % dextran sulfate, 100 μg/ml salmon sperm DNA, and ^{32}p labeled probe and wash at 68 °C with 3 x SSC and 0.1 % SDS.

11. The recombinant protein of claim 8, wherein the protein is encoded by a polynucleotide at least 60 % identical with SEQ ID NOs: 9, 13, 42, 43 or portions thereof as determined using the Bestfit procedure of the DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the university of Wisconsin (gap creation penalty - 12, gap extension penalty - 4).

12. A pharmaceutical composition comprising, as an active ingredient, the recombinant protein of claim 8.

13. A method of identifying a chromosome region harboring a heparanase gene in a chromosome spread comprising the steps of:

(a) hybridizing the chromosome spread with a tagged polynucleotide probe encoding heparanase;

(b) washing the chromosome spread, thereby removing excess of non-hybridized probe; and

(c) searching for signals associated with said hybridized tagged polynucleotide probe, wherein detected signals being indicative of a chromosome region harboring a heparanase gene.